



SEQUENCE LISTING

<110> Kalluri, Raghuram

<120> Anti-Angiogenic Proteins and Fragments and Methods of Use Thereof

<130> 02312/2085B (formerly 1440.1027-005)

<140> US 09/543,371

<141> 2000-04-04

<150> US 60/089,689

<151> 1998-06-17

<150> US 60/126,175

<151> 1999-03-25

<150> US 09/335,224

<151> 1999-06-17

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 690

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(687)

<223>

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Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp
1 5 10 15

48

gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac tct
Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
20 25 30

96

ttg ctc tac gtg caa ggc aat gaa cgg gcc cat gga cag gac ttg ggc
Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
35 40 45

144

acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg ttc
Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
50 55 60

192

tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac tcg
Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
65 70 75 80

240

tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc atc
Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile

288

85	90	95	
acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt gag Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu 100	105	110	336
gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc cca Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro 115	120	125	384
ccg tgc ccc agc ggg tgg tcc tcg ctg tgg atc ggc tac tct ttt gtg Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val 130	135	140	432
atg cac acc agc gct gca gaa ggc tct ggc caa gcc ctg gcg tcc Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser 145	150	155	480
ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag tgt Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys 165	170	175	528
cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt tgg His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp 180	185	190	576
ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg tcc Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser 195	200	205	624
acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa gtc Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val 210	215	220	672
tgt atg aga aga aca taa Cys Met Arg Arg Thr 225			690

<210> 2
<211> 229
<212> PRT
<213> Homo sapiens

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Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly			
35	40	45	

Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
50 55 60

Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
65 70 75 80

Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
85 90 95

Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
100 105 110

Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
115 120 125

Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
130 135 140

Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
145 150 155 160

Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
165 170 175

His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
180 185 190

Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
195 200 205

Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
210 215 220

Cys Met Arg Arg Thr
225

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<212> DNA
<213> Artificial sequence

<220>
<223> pET22b(+) forward oligonucleotide primer for Arresten

<400> 3
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<222> (1)..(681)
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1 5 10 15

48

ccc atg tgc ccg gtg ggc atg aac aaa ctc tgg agt gga tac agc ctg
Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
20 25 30

96

ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg
Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
35 40 45

144

gcg ggc tcc tgc ctg gcg cgg ttc agc acc atg ccc ttc ctg tac tgc
Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
50 55 60

192

aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac
Asn Pro Gly Asp Val Cys Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
65 70 75 80

240

tgg ctc tct acc act gcg ccg ctg ccc atg atg ccc gtg gcc gag gac
Trp Leu Ser Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
85 90 95

288

gag atc aag ccc tac atc agc cgc tgt tct gtg tgt gag gcc ccg gcc
Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
100 105 110

336

atc gcc atc gcg gtc cac agt cag gat gtc tcc atc cca cac tgc cca
Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro

384

115	120	125	
gct ggg tgg cgg agt ttg tgg atc gga tat tcc ttc ctc atg cac acg Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr			432
130	135	140	
gcg gcg gga gac gaa ggc ggt ggc caa tca ctg gtg tca ccg ggc agc Ala Ala Gly Asp Glu Gly Gly Gln Ser Leu Val Ser Pro Gly Ser			480
145	150	155	160
tgt cta gag gac ttc cgc gcc aca cca ttc atc gaa tgc aat gga ggc Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly			528
165	170	175	
cgc ggc acc tgc cac tac tac gcc aac aag tac agc ttc tgg ctg acc Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr			576
180	185	190	
acc att ccc gag cag agc ttc cag ggc tcg ccc tcc gcc gac acg ctc Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu			624
195	200	205	
aag gcc ggc ctc atc cgc aca cac atc agc cgc tgc cag gtg tgc atg Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met			672
210	215	220	
aag aac ctg tga Lys Asn Leu			684
225			
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Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu			
35	40	45	
Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys			
50	55	60	
Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr			
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Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
85 90 95

Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
100 105 110

Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
115 120 125

Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
130 135 140

Ala Ala Gly Asp Glu Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
145 150 155 160

Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
165 170 175

Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
180 185 190

Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
195 200 205

Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
210 215 220

Lys Asn Leu
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<210> 7
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<212> DNA
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<220>
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<223> Tumstatin 333

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<223> Tumstatin 334

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Gly Leu Lys Gly Lys Arg Gly Asp Ser Gly Ser Pro Ala Thr Trp Thr
1 5 10 15

48

acg aga ggc ttt gtc ttc acc cga cac agt caa acc aca gca att cct
Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile Pro
20 25 30

96

tca tgt cca gag ggg aca gtg cca ctc tac agt ggg ttt tct ttt ctt
Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
35 40 45

144

ttt gta caa gga aat caa cga gcc cac gga caa gac ctt gga act ctt
Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
50 55 60

192

ggc agc tgc ctg cag cga ttt acc aca atg cca ttc tta ttc tgc aat
Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
65 70 75 80

240

gtc aat gat gta tgt aat ttt gca tct cga aat gat tat tca tac tgg		288	
Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp			
85	90	95	
ctg tca aca cca gct ctg atg cca atg aac atg gct ccc att act ggc		336	
Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly			
100	105	110	
aga gcc ctt gag cct tat ata agc aga tgc act gtt tgt gaa ggt cct		384	
Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro			
115	120	125	
gcg atc gcc ata gcc gtt cac agc caa acc act gac att cct cca tgt		432	
Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys			
130	135	140	
cct cac ggc tgg att tct ctc tgg aaa gga ttt tca ttc atc atg ttc		480	
Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe			
145	150	155	160
aca agt gca ggt tct gag ggc acc ggg caa gca ctg gcc tcc cct ggc		528	
Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly			
165	170	175	
tcc tgc ctg gaa gaa ttc cga gcc agc cca ttt cta gaa tgt cat gga		576	
Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly			
180	185	190	
aga gga acg tgc aac tac tat tca aat tcc tac agt ttc tgg ctg gct		624	
Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala			
195	200	205	
tca tta aac cca gaa aga atg ttc aga aag cct att cca tca act gtg		672	
Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val			
210	215	220	
aaa gct ggg gaa tta gaa aaa ata ata agt cgc tgt cag gtg tgc atg		720	
Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met			
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Lys Lys Arg His			

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<222> (1)..(372)
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<223> Tumstatin 334

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20 25 30

Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
35 40 45

Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
50 55 60

Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
65 70 75 80

Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
85 90 95

Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly
100 105 110

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
115 120 125

Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys
130 135 140

Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe
145 150 155 160

Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly
165 170 175

Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly
180 185 190

Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala
195 200 205

Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val
210 215 220

Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met
225 230 235 240

Lys Lys Arg His

<210> 11
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<212> DNA
<213> Artificial sequence

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<223> primer

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<210> 13
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1 5

<210> 14
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<212> PRT
<213> Artificial sequence

<220>
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Lys Leu Ala Ala Ala Leu Glu
1 5

<210> 15
<211> 28
<212> DNA
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<220>
<223> pPICZaA forward oligonucleotide primer for Arresten

<400> 15
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<210> 16
<211> 35
<212> DNA
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<223> pPICZaA reverse oligonucleotide primer for Arresten

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<210> 17
<211> 31
<212> DNA
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<223> pPICZaA forward oligonucleotide primer for Canstatin

<400> 17
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<223> pPICZaA reverse oligonucleotide primer for Canstatin

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32